ONLINE SUPPLEMENTARY MATERIAL

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2 Of the 15 single nucleotide disagreements between our de novo NR1 sequence 3 and the GenBank R100 sequence (Table 4), nine arise from an eleventh OOP repeat near 4 the carboxy-terminus of the transfer protein TraD in the de novo NR1 sequence. TraD 5 proteins, which function as inner membrane ATPases, of other E. coli and Salmonella 6 plasmids (e.g., NC_005327, NC_006671, NC_006855) have a variable number of QQP 7 repeats, suggesting that this is a real polymorphism. 8 Another disagreement is a single base change within codon 301 of the mating pair 9 stabilization protein TraN. The *de novo* NR1 encodes glutamate (GAA), but the GenBank 10 R100 encodes a stop codon (TAA). The traN gene of R100-1, a derepressed variant of R100 with a mutation in finO, has also been sequenced and has a glutamate at the 12 corresponding position (5), supporting the accuracy of our NR1 sequence at this position. 13 NR1 is conjugative (unpublished observations), which further supports the functionality 14 of TraN. 15 The remaining five disagreements are within a \sim 1400 bp region of IS10-R of 16 Tn10, which contains the functional transposase of this composite transposon (4), and the 17 3' flanking sequence. Three are synonymous third base substitutions in the IS10-R 18 transposase, two of which (NR1 ATCile:R100 ATTile; NR1 CGGarg:R100 CGAarg) are 19 identical to the corresponding positions in IS 10-L as previously reported (4). The third 20 (NR1 GCAala:R100 GCCala) is identical to the corresponding position in the previously 21 reported IS10-R (4), whereas the GenBank R100 sequence agrees with IS10-L (4). A 22 fourth disagreement in the ~1400 bp region is within yefA, a hypothetical protein near 23 IS10-R but outside Tn10. This conservative substitution (NR1 TTCphe:R100 TACtyr)

was previously observed in *yefA* of plasmids F and R6-5 (3). The last disagreement in the ~1400 bp region is in the plasmid SOS inhibition protein PsiB, which is proposed to prevent induction of the bacterial SOS response during conjugative transfer in order to protect single-stranded plasmid DNA (1). The NR1 sequence has a single nucleotide deletion in codon 127 of PsiB, resulting in a frameshift and premature termination. This *psiB* polymorphism is in the C-terminal region, which when deleted in other examples of this gene does not affect the protein's activity (2).

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Table 4. Disagreements between de novo NR1 sequence and R100 reference sequence

Number of disagreements	Location	Туре
9	TraD	additional QQP repeat in
		NR1 sequence
1	TraN	NR1 GAA glu: R100 TAA
		stop
3	IS10-R transposase	synonymous 3 rd base
		substitutions
1	yefA, hypothetical protein	conservative amino acid
		substitution
1	PsiB	1 nt deletion resulting in
		frameshift and premature
		termination